

## SEQUENCE LISTING

<110> Sheppard, Paul O.  
 Deisher, Theresa A.  
 Jaspers, Stephen R.  
 Bishop, Paul D.  
  
 <120> TML Polynucleotides  
  
 <130> 97-04D3  
  
 <150> 09/404, 417  
 <151> 1999-09-23  
  
 <150> 09/046, 479  
 <151> 1998-03-28  
  
 <150> 60/041, 102  
 <151> 1997-03-24  
  
 <160> 13  
  
 <170> FastSEQ for Windows Version 4.0  
  
 <210> 1  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1)...(351)  
  
 <400> 1

atg ccc tcc cca ggg acc gtc tgc agc ctc ctg ctc ctc ggc atg ctc	48
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu	
1 5 10 15	
tgg ctg gac ttg gcc atg gca ggc tcc agc ttc ctg agc cct gaa cac	96
Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His	
20 25 30	
cag aga gtc cag cag aga aag gag tcg aag aag cca cca gcc aag ctg	144
Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu	
35 40 45	
cag ccc cga gct cta gca ggc tgg ctc cgc ccg gaa gat gga ggt caa	192
Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln	
50 55 60	
gca gaa ggg gca gag gat gaa ctg gaa gtc cgg ttc aac gcc ccc ttt	240
Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe	
65 70 75 80	
gat gtt gga atc aag ctg tca ggg gtt cag tac cag cag cac agc cag	288
Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln	
85 90 95	
gcc ctg ggg aag ttt ctt cag gac atc ctc tgg gaa gag gcc aaa gag	336

Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu																																																																																																			
100	105	110		gcc cca gcc gac aag	351	Ala Pro Ala Asp Lys		115		<210> 2		<211> 117		<212> PRT		<213> Homo sapiens		<400> 2		Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu		1 5 10 15		Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His		20 25 30		Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu		35 40 45		Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln		50 55 60		Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe		65 70 75 80		Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln		85 90 95		Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu		100 105 110		Ala Pro Ala Asp Lys		115		<210> 3		<211> 546		<212> DNA		<213> Sus scrofa		<220>		<221> CDS		<222> (40) ... (396)		<400> 3		gggcagagac acacacgcgc ccagttgtcc agctccagg atg gtg tcc cgc aag	54	Met Val Ser Arg Lys		1 5		gct gtg gtc ctg ctg gtg cac gca gct gcc atg ctg gcc tcc	102	Ala Val Val Val Leu Leu Val Val His Ala Ala Ala Met Leu Ala Ser		10 15 20		cac acg gaa gcc ttt gtt ccc agc ttt acc tac ggg gaa ctt cag agg	150	His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr Gly Glu Leu Gln Arg		25 30 35		atg cag gaa aag gag cgg aat aaa ggg caa aag aaa tcc ctg agt gtc	198	Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys Ser Leu Ser Val		40 45 50		cag cag gcg tcg gag gag ctc ggc cct ctg gac ccc tcg gag ccc acg	246	Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp Pro Ser Glu Pro Thr		55 60 65		aag gaa gaa agg gtg gtt atc aag ctg ctc gcg cct gtg gac att	294
110																																																																																																			
gcc cca gcc gac aag	351																																																																																																		
Ala Pro Ala Asp Lys																																																																																																			
115																																																																																																			
<210> 2																																																																																																			
<211> 117																																																																																																			
<212> PRT																																																																																																			
<213> Homo sapiens																																																																																																			
<400> 2																																																																																																			
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu																																																																																																			
1 5 10 15																																																																																																			
Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His																																																																																																			
20 25 30																																																																																																			
Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu																																																																																																			
35 40 45																																																																																																			
Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln																																																																																																			
50 55 60																																																																																																			
Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe																																																																																																			
65 70 75 80																																																																																																			
Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln																																																																																																			
85 90 95																																																																																																			
Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu																																																																																																			
100 105 110																																																																																																			
Ala Pro Ala Asp Lys																																																																																																			
115																																																																																																			
<210> 3																																																																																																			
<211> 546																																																																																																			
<212> DNA																																																																																																			
<213> Sus scrofa																																																																																																			
<220>																																																																																																			
<221> CDS																																																																																																			
<222> (40) ... (396)																																																																																																			
<400> 3																																																																																																			
gggcagagac acacacgcgc ccagttgtcc agctccagg atg gtg tcc cgc aag	54																																																																																																		
Met Val Ser Arg Lys																																																																																																			
1 5																																																																																																			
gct gtg gtc ctg ctg gtg cac gca gct gcc atg ctg gcc tcc	102																																																																																																		
Ala Val Val Val Leu Leu Val Val His Ala Ala Ala Met Leu Ala Ser																																																																																																			
10 15 20																																																																																																			
cac acg gaa gcc ttt gtt ccc agc ttt acc tac ggg gaa ctt cag agg	150																																																																																																		
His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr Gly Glu Leu Gln Arg																																																																																																			
25 30 35																																																																																																			
atg cag gaa aag gag cgg aat aaa ggg caa aag aaa tcc ctg agt gtc	198																																																																																																		
Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys Ser Leu Ser Val																																																																																																			
40 45 50																																																																																																			
cag cag gcg tcg gag gag ctc ggc cct ctg gac ccc tcg gag ccc acg	246																																																																																																		
Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp Pro Ser Glu Pro Thr																																																																																																			
55 60 65																																																																																																			
aag gaa gaa agg gtg gtt atc aag ctg ctc gcg cct gtg gac att	294																																																																																																		

Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu Ala Pro Val Asp Ile			
70	75	80	85
gga atc agg atg gac tcc agg cag ctg gaa aag tac cgg gcc acc ctg			342
Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys Tyr Arg Ala Thr Leu			
90	95	100	
gaa agg ctg ctg ggc cag gcg ccg cag tcc acc cag aac cag aat gcc			390
Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr Gln Asn Gln Asn Ala			
105	110	115	
gcc aag taacaggccg ctgggggaga aggaggacac agctcggacc cccctccac			446
Ala Lys			
gcagggaggg cctagaaaatc cgctgggctt ggaaggaaaa caccctctcc caaacagccc			506
tcagcccccc tccccccagca aataaagcgt ggaaataggc			546
<210> 4			
<211> 119			
<212> PRT			
<213> Sus scrofa			
<400> 4			
Met Val Ser Arg Lys Ala Val Val Val Leu Leu Val Val His Ala Ala			
1	5	10	15
Ala Met Leu Ala Ser His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr			
20	25	30	
Gly Glu Leu Gln Arg Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys			
35	40	45	
Lys Ser Leu Ser Val Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp			
50	55	60	
Pro Ser Glu Pro Thr Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu			
65	70	75	80
Ala Pro Val Asp Ile Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys			
85	90	95	
Tyr Arg Ala Thr Leu Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr			
100	105	110	
Gln Asn Gln Asn Ala Ala Lys			
115			
<210> 5			
<211> 6			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Artificial peptide			
<221> VARIANT			
<222> (2)...(2)			
<223> Xaa is any amino acid			
<221> VARIANT			
<222> (5)...(5)			
<223> Xaa is any amino acid			
<221> VARIANT			
<222> (1)...(6)			
<223> Xaa = Any Amino Acid			
<221> VARIANT			
<222> (1)...(6)			

```

<223> Xaa = Any Amino Acid

<400> 5
Glu Xaa Gln Arg Xaa Gln
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial peptide

<221> VARIANT
<222> (3)...(3)
<223> Xaa is any amino acid

<221> VARIANT
<222> (5)...(5)
<223> Xaa is any amino acid

<221> VARIANT
<222> (1)...(7)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (1)...(7)
<223> Xaa = Any Amino Acid

<400> 6
Ala Pro Xaa Asp Xaa Gly Ile
1 5

<210> 7
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 7
ttcttcgact cctttctctg ctggactctc tgggtttcag 40
<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 8
catgctctgg ctggactt 18
<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> OLIGONUCLEOTIDE

<400> 9
ctggactctc tgggtttc 18

<210> 10
<211> 54
<212> DNA
<213> Homo sapiens

<400> 10
ggctccagct tcctgagccc tgaacaccag agagtccagc agagaaagga gtcg 54

<210> 11
<211> 18
<212> PRT
<213> Homo sapiens

<400> 11
Gly Ser Ser Phe Leu Ser Pro Glu His Gln Arg Val Gln Gln Arg Lys
 1           5           10          15
Glu Ser

<210> 12
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (2)...(2)
<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (3)...(3)
<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (4)...(4)
<223> Xaa is Phe, Trp, Tyr, Leu, Val, or Ile

<221> VARIANT
<222> (5)...(5)
<223> Xaa is Phe, Tyr, Leu, Val, or Ile

<221> VARIANT
<222> (6)...(6)
<223> Xaa is Gly, Ser, Ala, Thr, Met, or Pro

<221> VARIANT
<222> (7)...(7)
<223> Xaa is Gly, Pro, Ala, Ile, leu or Val

<221> VARIANT
<222> (8)...(8)
<223> Xaa is Glu or Asp

```

```

<221> VARIANT
<222> (9)...(9)
<223> Xaa is His, Arg, Lys, Phe, or Tyr

<221> VARIANT
<222> (10)...(10)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (11)...(11)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (12)...(12)
<223> Xaa is Met, Val, Leu, Ile, Trp, or Phe

<221> VARIANT
<222> (13)...(13)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (14)...(14)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (15)...(15)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (16)...(16)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (17)...(17)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<221> VARIANT
<222> (18)...(18)
<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<400> 12
Xaa Xaa
      1           5           10          15
Xaa Xaa

<210> 13
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial peptide

```

<400> 13  
Ser Leu Ser Arg Gln Gly Ser His Gln Phe Pro Gln Glu Val  
1 5 10